

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Dalla-Favera, Riccardo  
Chaganti, Raju S.K.
- (ii) TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS  
bcl-6
- (iii) NUMBER OF SEQUENCES: 9
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Cooper & Dunham LLP
  - (B) STREET: 1185 Avenue of the Americas
  - (C) CITY: New York
  - (D) STATE: New York
  - (E) COUNTRY: United States of America
  - (F) ZIP: 10036
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: White, John P.
  - (B) REGISTRATION NUMBER: 28,678
  - (C) REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US-Y
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (212) 278-0400
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3720 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 328..2445
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCCCCTCGA GCCTCGAACCC GGAACCTCCA AATCCGAGAC GCTCTGCTTA TGAGGACCTC	60
GAAATATGCC GGCCAGTGAA AAAATCTTAT GGCTTTGAGG GCTTTGGTT GGCCAGGGC	120

AGTAAAAATC TCGGAGAGCT GACACCAAGT CCTCCCTGC CACGTAGCAG TGGTAAAGTC	180
CGAAGCTCAA ATTCCGAGAA TTGAGCTCTG TTGATTCTTA GAACTGGGT TCTTAGAAGT	240
GGTGATGCAA GAAGTTCTA GGAAAGGCCG GACACCAGGT TTTGAGCAAA ATTTTGGACT	300
GTGAAGCAAG GCATTGGTGA AGACAAA ATG GCC TCG CCG GCT GAC AGC TGT Met Ala Ser Pro Ala Asp Ser Cys	351
1 5	
ATC CAG TTC ACC CGC CAT GCC AGG GAT GTT CTT CTC AAC CTT AAT CGT Ile Gln Phe Thr Arg His Ala Arg Asp Val Leu Leu Asn Leu Asn Arg	399
10 15 20	
CTC CGG AGT CGA GAC ATC TTG ACT GAT GTT GTC ATT GTT GTG AGC CGT Leu Arg Ser Arg Asp Ile Leu Thr Asp Val Val Ile Val Val Ser Arg	447
25 30 35 40	
GAG CAG TTT AGA GCC CAT AAA ACG GTC CTC ATG GCC TGG AGA GGC CTG Glu Gln Phe Arg Ala His Lys Thr Val Leu Met Ala Trp Arg Gly Leu	495
45 50 55	
TTC TAT AGC ATC TTT ACA GAC CAG TTG AAA TGC AAC CTT AGT GTG ATC Phe Tyr Ser Ile Phe Thr Asp Gln Leu Lys Cys Asn Leu Ser Val Ile	543
60 65 70	
AAT CTA GAT CCT GAG ATC AAC CCT GAG GGA TTC TGC ATC CTC CTG GAC Asn Leu Asp Pro Glu Ile Asn Pro Glu Gly Phe Cys Ile Leu Leu Asp	591
75 80 85	
TTC ATG TAC ACA TCT CGG CTC AAT TTG CGG GAG GGC AAC ATC ATG GCT Phe Met Tyr Thr Ser Arg Leu Asn Leu Arg Glu Gly Asn Ile Met Ala	639
90 95 100	
GTG ATG GCC ACG GCT ATG TAC CTG CAG ATG GAG CAT GTT GTG GAC ACT Val Met Ala Thr Ala Met Tyr Leu Gln Met Glu His Val Val Asp Thr	687
105 110 115 120	
GTC CGG AAG TTT ATT AAG GCC AGT GAA GCA GAG ATG GTT TCT GCC ATC Cys Arg Lys Phe Ile Lys Ala Ser Glu Ala Glu Met Val Ser Ala Ile	735
125 130 135	
AAG CCT CCT CGT GAA GAG TTC CTC AAC AGC CGG ATG CTG ATG CCC CAA Lys Pro Pro Arg Glu Glu Phe Leu Asn Ser Arg Met Leu Met Pro Gln	783
140 145 150	
GAC ATC ATG GCC TAT CGG GGT CGT GAG GTG GTG GAG AAC AAC CTG CCA Asp Ile Met Ala Tyr Arg Gly Arg Glu Val Val Glu Asn Asn Leu Pro	831
155 160 165	
CTG AGG AGC GCC CCT GGG TGT GAG AGC AGA GCC TTT GCC CCC AGC CTG Leu Arg Ser Ala Pro Gly Cys Glu Ser Arg Ala Phe Ala Pro Ser Leu	879
170 175 180	
TAC AGT GGC CTG TCC ACA CCG CCA GCC TCT TAT TCC ATG TAC AGC CAC Tyr Ser Gly Leu Ser Thr Pro Pro Ala Ser Tyr Ser Met Tyr Ser His	927
185 190 195 200	
CTC CCT GTC AGC AGC CTC CTC TTC TCC GAT GAG GAG TTT CGG GAT GTC Leu Pro Val Ser Ser Leu Leu Phe Ser Asp Glu Glu Phe Arg Asp Val	975
205 210 215	

CGG ATG CCT GTG GCC AAC CCC TTC CCC AAG GAG CGG GCA CTC CCA TGT Arg Met Pro Val Ala Asn Pro Phe Pro Lys Glu Arg Ala Leu Pro Cys 220 225 230	1023
GAT AGT GCC AGG CCA GTC CCT GGT GAG TAC AGC CGG CCG ACT TTG GAG Asp Ser Ala Arg Pro Val Pro Gly Glu Tyr Ser Arg Pro Thr Leu Glu 235 240 245	1071
GTG TCC CCC AAT GTG TGC CAC AGC AAT ATC TAT TCA CCC AAG GAA ACA Val Ser Pro Asn Val Cys His Ser Asn Ile Tyr Ser Pro Lys Glu Thr 250 255 260	1119
ATC CCA GAA GAG GCA CGA AGT GAT ATG CAC TAC AGT GTG GCT GAG GGC Ile Pro Glu Glu Ala Arg Ser Asp Met His Tyr Ser Val Ala Glu Gly 265 270 275 280	1167
CTC AAA CCT GCT GCC CCC TCA GCC CGA AAT GCC CCC TAC TTC CCT TGT Leu Lys Pro Ala Ala Pro Ser Ala Arg Asn Ala Pro Tyr Phe Pro Cys 285 290 295	1215
GAC AAG GCC AGC AAA GAA GAA GAG AGA CCC TCC TCG GAA GAT GAG ATT Asp Lys Ala Ser Lys Glu Glu Glu Arg Pro Ser Ser Glu Asp Glu Ile 300 305 310	1263
GCC CTG CAT TTC GAG CCC CCC AAT GCA CCC CTG AAC CGG AAG GGT CTG Ala Leu His Phe Glu Pro Pro Asn Ala Pro Leu Asn Arg Lys Gly Leu 315 320 325	1311
GTT AGT CCA CAG AGC CCC CAG AAA TCT GAC TGC CAG CCC AAC TCG CCC Val Ser Pro Gln Ser Pro Gln Lys Ser Asp Cys Gln Pro Asn Ser Pro 330 335 340	1359
ACA GAG GCC TGC AGC AGT AAG AAT GCC TGC ATC CTC CAG GGT TCT GGC Thr Glu Ala Cys Ser Ser Lys Asn Ala Cys Ile Leu Gln Gly Ser Gly 345 350 355 360	1407
TCC CCT CCA GCC AAG AGC CCC ACT GAC CCC AAA GCC TGC AGC TGG AAG Ser Pro Pro Ala Lys Ser Pro Thr Asp Pro Lys Ala Cys Ser Trp Lys 365 370 375	1455
AAA TAC AAG TTC ATC GTG CTC AAC AGC CTC AAC CAG AAT GCC AAA CCA Lys Tyr Lys Phe Ile Val Leu Asn Ser Leu Asn Gln Asn Ala Lys Pro 380 385 390	1503
GGG GGG CCT GAG CAG GCT GAG CTG GGC CGC CTT TCC CCA CGA GCC TAC Gly Gly Pro Glu Gln Ala Glu Leu Gly Arg Leu Ser Pro Arg Ala Tyr 395 400 405	1551
ACG GCC CCA CCT GCC TGC CAG CCA CCC ATG GAG CCT GAG AAC CTT GAC Thr Ala Pro Pro Ala Cys Gln Pro Pro Met Glu Pro Glu Asn Leu Asp 410 415 420	1599
CTC CAG TCC CCA ACC AAG CTG AGT GCC AGC GGG GAG GAC TCC ACC ATC Leu Gln Ser Pro Thr Lys Leu Ser Ala Ser Gly Glu Asp Ser Thr Ile 425 430 435 440	1647
CCA CAA GCC AGC CGG CTC AAT AAC ATC GTT AAC AGG TCC ATG ACG GGC Pro Gln Ala Ser Arg Leu Asn Asn Ile Val Asn Arg Ser Met Thr Gly 445 450 455	1695
TCT CCC CGC AGC AGC GAG AGC CAC TCA CCA CTC TAC ATG CAC CCC Ser Pro Arg Ser Ser Glu Ser His Ser Pro Leu Tyr Met His Pro	1743

460	465	470	
CCG AAG TGC ACG TCC TGC GGC TCT CAG TCC CCA CAG CAT GCA GAG ATG Pro Lys Cys Thr Ser Cys Gly Ser Gln Ser Pro Gln His Ala Glu Met 475	480	485	1791
TGC CTC CAC ACC GCT GGC CCC ACG TTC GCT GAG GAG ATG GGA GAG ACC Cys Leu His Thr Ala Gly Pro Thr Phe Ala Glu Glu Met Gly Glu Thr 490	495	500	1839
CAG TCT GAG TAC TCA GAT TCT AGC TGT GAG AAC GGG GCC TTC TTC TGC Gln Ser Glu Tyr Ser Asp Ser Ser Cys Glu Asn Gly Ala Phe Phe Cys 505	510	515	1887
AAT GAG TGT GAC TGC CGC TTC TCT GAG GAG GCC TCA CTC AAG AGG CAC Asn Glu Cys Asp Cys Arg Phe Ser Glu Glu Ala Ser Leu Lys Arg His 525	530	535	1935
ACG CTG CAG ACC CAC AGT GAC AAA CCC TAC AAG TGT GAC CGC TGC CAG Thr Leu Gln Thr His Ser Asp Lys Pro Tyr Lys Cys Asp Arg Cys Gln 540	545	550	1983
GCC TCC TTC CGC TAC AAG GGC AAC CTC GCC AGC CAC AAG ACC GTC CAT Ala Ser Phe Arg Tyr Lys Gly Asn Leu Ala Ser His Lys Thr Val His 555	560	565	2031
ACC GGT GAG AAA CCC TAT CGT TGC AAC ATC TGT GGG GCC CAG TTC AAC Thr Gly Glu Lys Pro Tyr Arg Cys Asn Ile Cys Gly Ala Gln Phe Asn 570	575	580	2079
CGG CCA GCC AAC CTG AAA ACC CAC ACT CGA ATT CAC TCT GGA GAG AAG Arg Pro Ala Asn Leu Lys Thr His Thr Arg Ile His Ser Gly Glu Lys 585	590	595	2127
CCC TAC AAA TGC GAA ACC TGC GGA GCC AGA TTT GTA CAG GTG GCC CAC Pro Tyr Lys Cys Glu Thr Cys Gly Ala Arg Phe Val Gln Val Ala His 605	610	615	2175
CTC CGT GCC CAT GTG CTT ATC CAC ACT GGT GAG AAG CCC TAT CCC TGT Leu Arg Ala His Val Leu Ile His Thr Gly Glu Lys Pro Tyr Pro Cys 620	625	630	2223
GAA ATC TGT GGC ACC CGT TTC CGG CAC CTT CAG ACT CTG AAG AGC CAC Glu Ile Cys Gly Thr Arg Phe Arg His Leu Gln Thr Leu Lys Ser His 635	640	645	2271
CTG CGA ATC CAC ACA GGA GAG AAA CCT TAC CAT TGT GAG AAG TGT AAC Leu Arg Ile His Thr Gly Glu Lys Pro Tyr His Cys Glu Lys Cys Asn 650	655	660	2319
CTG CAT TTC CGT CAC AAA AGC CAG CTG CGA CTT CAC TTG CGC CAG AAG Leu His Phe Arg His Lys Ser Gln Leu Arg Leu His Leu Arg Gln Lys 665	670	675	2367
CAT GGC GCC ATC ACC AAC ACC AAG GTG CAA TAC CGC GTG TCA GCC ACT His Gly Ala Ile Thr Asn Thr Lys Val Gln Tyr Arg Val Ser Ala Thr 685	690	695	2415
GAC CTG CCT CCG GAG CTC CCC AAA GCC TGC TGAAGCATGG AGTGTGATG Asp Leu Pro Pro Glu Leu Pro Lys Ala Cys 700	705		2465

CTTCGTCTC CAGCCCTTC TCAGAACATCA CCCAAAGGAT ACTGTAACAC TTTACAATGT	2525
TCATCCCAGT ATGTAGTGCC TCTTCATCC ACTAGTCAA ATCATAGCTG GGGGTTGGGG	2585
GTGGTGGGGG TCAGGGGCCTG GGGGACTGGG AGCCGCAGCA GCTCCCCCTC CCCCACGTCC	2645
ATAAAACATT AAGAAAATCA TATTGCTTCT TCTCCTATGT GNNNNNNNNN NNNNNNNNNN	2705
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	2765
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	2825
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	2885
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	2945
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	3005
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	3065
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	3125
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	3185
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	3245
NTTTAAGTAT TGCACTGTAA TAAGTAAGAA AATATTTGT CTAAATGCC TCAGTGTATT	3305
TGTATTTTT TGCAAGTGGG GGGTTACAAT TTACCCAGTG TGTATTAAAA AAAACCCAAA	3365
GAACCCAAAA ATCTCAGAA GGAAAAATGT GTAATTTGT TCTAGTTTC AGTTGTATA	3425
TACCCGTACA ACGTGTCTC ACGGTGCCTT TTTCACGGA AGTTTCAAT GATGGCGAG	3485
CGTGCACCAT CCCTTTTGAA AGTGTAGGCA GACACAGGAA CTTGAAGTTG TTACTAACTA	3545
AACTCTCTT GGGAAATGTT GTCTCATCCC ANTCTGCGTC ATGCTTGTGT GATAACTACT	3605
CCGGAGACAG GGTTGGCTG TGTCTAAACT GCATTACCGC GTTGTAAAAA ATAGCTGTAC	3665
CAATATAAGA ATAAAATGTT GGAAAGTCGC AAAAAAAAAA AAAAAAAAAA AAAAAA	3720

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 706 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Ser Pro Ala Asp Ser Cys Ile Gln Phe Thr Arg His Ala Arg  
1 5 10 15

Asp Val Leu Leu Asn Leu Asn Arg Leu Arg Ser Arg Asp Ile Leu Thr  
20 25 30

Asp Val Val Ile Val Val Ser Arg Glu Gln Phe Arg Ala His Lys Thr  
35 40 45

Val Leu Met Ala Trp Arg Gly Leu Phe Tyr Ser Ile Phe Thr Asp Gln  
50 55 60

Leu Lys Cys Asn Leu Ser Val Ile Asn Leu Asp Pro Glu Ile Asn Pro  
65 70 75 80

Glu Gly Phe Cys Ile Leu Leu Asp Phe Met Tyr Thr Ser Arg Leu Asn  
85 90 95

Leu Arg Glu Gly Asn Ile Met Ala Val Met Ala Thr Ala Met Tyr Leu  
100 105 110

Gln Met Glu His Val Val Asp Thr Cys Arg Lys Phe Ile Lys Ala Ser  
115 120 125

Glu Ala Glu Met Val Ser Ala Ile Lys Pro Pro Arg Glu Glu Phe Leu  
130 135 140

Asn Ser Arg Met Leu Met Pro Gln Asp Ile Met Ala Tyr Arg Gly Arg  
145 150 155 160

Glu Val Val Glu Asn Asn Leu Pro Leu Arg Ser Ala Pro Gly Cys Glu  
165 170 175

Ser Arg Ala Phe Ala Pro Ser Leu Tyr Ser Gly Leu Ser Thr Pro Pro  
180 185 190

Ala Ser Tyr Ser Met Tyr Ser His Leu Pro Val Ser Ser Leu Leu Phe  
195 200 205

Ser Asp Glu Glu Phe Arg Asp Val Arg Met Pro Val Ala Asn Pro Phe  
210 215 220

Pro Lys Glu Arg Ala Leu Pro Cys Asp Ser Ala Arg Pro Val Pro Gly  
225 230 235 240

Glu Tyr Ser Arg Pro Thr Leu Glu Val Ser Pro Asn Val Cys His Ser  
245 250 255

Asn Ile Tyr Ser Pro Lys Glu Thr Ile Pro Glu Glu Ala Arg Ser Asp  
260 265 270

Met His Tyr Ser Val Ala Glu Gly Leu Lys Pro Ala Ala Pro Ser Ala  
275 280 285

Arg Asn Ala Pro Tyr Phe Pro Cys Asp Lys Ala Ser Lys Glu Glu Glu  
290 295 300

Arg Pro Ser Ser Glu Asp Glu Ile Ala Leu His Phe Glu Pro Pro Asn  
305 310 315 320

Ala Pro Leu Asn Arg Lys Gly Leu Val Ser Pro Gln Ser Pro Gln Lys  
325 330 335

Ser Asp Cys Gln Pro Asn Ser Pro Thr Glu Ala Cys Ser Ser Lys Asn  
340 345 350

Ala Cys Ile Leu Gln Gly Ser Gly Ser Pro Pro Ala Lys Ser Pro Thr  
355 360 365

Asp Pro Lys Ala Cys Ser Trp Lys Lys Tyr Lys Phe Ile Val Leu Asn

370

375

380

Ser Leu Asn Gln Asn Ala Lys Pro Gly Gly Pro Glu Gln Ala Glu Leu  
385 390 395 400

Gly Arg Leu Ser Pro Arg Ala Tyr Thr Ala Pro Pro Ala Cys Gln Pro  
405 410 415

Pro Met Glu Pro Glu Asn Leu Asp Leu Gln Ser Pro Thr Lys Leu Ser  
420 425 430

Ala Ser Gly Glu Asp Ser Thr Ile Pro Gln Ala Ser Arg Leu Asn Asn  
435 440 445

Ile Val Asn Arg Ser Met Thr Gly Ser Pro Arg Ser Ser Ser Glu Ser  
450 455 460

His Ser Pro Leu Tyr Met His Pro Pro Lys Cys Thr Ser Cys Gly Ser  
465 470 475 480

Gln Ser Pro Gln His Ala Glu Met Cys Leu His Thr Ala Gly Pro Thr  
485 490 495

Phe Ala Glu Glu Met Gly Glu Thr Gln Ser Glu Tyr Ser Asp Ser Ser  
500 505 510

Cys Glu Asn Gly Ala Phe Phe Cys Asn Glu Cys Asp Cys Arg Phe Ser  
515 520 525

Glu Glu Ala Ser Leu Lys Arg His Thr Leu Gln Thr His Ser Asp Lys  
530 535 540

Pro Tyr Lys Cys Asp Arg Cys Gln Ala Ser Phe Arg Tyr Lys Gly Asn  
545 550 555 560

Leu Ala Ser His Lys Thr Val His Thr Gly Glu Lys Pro Tyr Arg Cys  
565 570 575

Asn Ile Cys Gly Ala Gln Phe Asn Arg Pro Ala Asn Leu Lys Thr His  
580 585 590

Thr Arg Ile His Ser Gly Glu Lys Pro Tyr Lys Cys Glu Thr Cys Gly  
595 600 605

Ala Arg Phe Val Gln Val Ala His Leu Arg Ala His Val Leu Ile His  
610 615 620

Thr Gly Glu Lys Pro Tyr Pro Cys Glu Ile Cys Gly Thr Arg Phe Arg  
625 630 635 640

His Leu Gln Thr Leu Lys Ser His Leu Arg Ile His Thr Gly Glu Lys  
645 650 655

Pro Tyr His Cys Glu Lys Cys Asn Leu His Phe Arg His Lys Ser Gln  
660 665 670

Leu Arg Leu His Leu Arg Gln Lys His Gly Ala Ile Thr Asn Thr Lys  
675 680 685

Val Gln Tyr Arg Val Ser Ala Thr Asp Leu Pro Pro Glu Leu Pro Lys  
690 695 700

Ala Cys  
705

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 103 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asp Gly Ser Phe Val Gln His Ser Val Arg Val Leu Gln Glu Leu Asn  
1 5 10 15

Lys Gln Arg Glu Lys Gly Gln Tyr Cys Asp Ala Thr Leu Asp Val Gly  
20 25 30

Gly Leu Val Phe Lys Ala His Trp Ser Val Leu Ala Cys Cys Ser His  
35 40 45

Phe Phe Gln Ser Leu Tyr Gly Asp Gly Ser Gly Ser Val Val Leu  
50 55 60

Pro Ala Gly Phe Ala Glu Ile Phe Gly Leu Leu Leu Asp Phe Phe Tyr  
65 70 75 80

Thr Gly His Leu Ala Leu Thr Ser Gly Asn Arg Asp Gln Val Leu Leu  
85 90 95

Ala Ala Arg Glu Leu Arg Val  
100

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 107 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asp Thr Ala Ser His Ser Leu Val Leu Leu Gln Gln Leu Asn Met  
1 5 10 15

Gln Arg Glu Phe Gly Phe Leu Cys Asp Cys Thr Val Ala Ile Gly Asp  
20 25 30

Val Tyr Phe Lys Ala His Arg Ala Val Leu Ala Ala Phe Ser Asn Tyr  
35 40 45  
Phe Lys Met Ile Phe Ile His Gln Thr Ser Glu Cys Ile Lys Ile Gln  
50 55 60  
Pro Thr Asp Ile Gln Pro Asp Ile Phe Ser Tyr Leu Leu His Ile Met  
65 70 75 80  
Tyr Thr Gly Lys Gly Pro Lys Gln Ile Val Asp His Ser Arg Leu Glu  
85 90 95  
Glu Gly Ile Arg Phe Leu His Ala Asp Tyr Leu  
100 105

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 106 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Asn Asn Ser Ser Glu Leu Ile Ala Val Ile Asn Gly Phe Arg Asn  
1 5 10 15

~~Ser Gly Arg Phe Cys Asp Ile Ser Ile Val Ile Asn Asp Glu Arg Ile~~  
20 25 30

~~Asn Ala His Lys Leu Ile Leu Ser Gly Ala Ser Glu Tyr Phe Ser Ile~~  
35 40 45

~~Leu Phe Ser Asn Asn Phe Ile Asp Ser Asn Glu Tyr Glu Val Asn Leu~~  
50 55 60

~~Ser His Leu Asp Tyr Gln Ser Val Asn Asp Leu Ile Asp Tyr Ile Tyr~~  
65 70 75 80

~~Gly Ile Pro Leu Ser Leu Thr Asn Asp Asn Val Lys Tyr Ile Leu Ser~~  
85 90 95

Thr Ala Asp Phe Leu Gln Ile Gly Ser Ala  
100 105

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 108 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Cys Leu Arg Trp Asn Asn His Gln Ser Asn Leu Leu Ser Val Phe Asp  
1 5 10 15

Gln Leu Leu His Ala Glu Thr Phe Thr Asp Val Thr Leu Ala Val Glu  
20 25 30

Gly Gln His Leu Lys Ala His Lys Asn Val Leu Ser Ala Cys Ser Pro  
35 40 45

Tyr Phe Asn Thr Leu Phe Val Ser His Pro Glu Lys His Pro Ile Val  
50 55 60

Ile Leu Lys Asp Val Pro Tyr Ser Asp Met Lys Ser Leu Leu Asp Phe  
65 70 75 80

Met Tyr Arg Gly Glu Val Ser Val Asp Gln Glu Arg Leu Thr Ala Phe  
85 90 95

Leu Arg Val Ala Glu Ser Leu Arg Ile Lys Gly Leu  
100 105

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 109 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gln Tyr Ser Asn Glu Gln His Thr Ala Arg Ser Phe Asp Ala Met Asn  
1 5 10 15

Glu Met Arg Lys Gln Lys Gln Leu Cys Asp Val Ile Leu Val Ala Asp  
20 25 30

Asp Val Glu Ile His Ala His Arg Met Val Leu Ala Ser Cys Ser Pro  
35 40 45

Tyr Phe Tyr Ala Met Phe Thr Ser Phe Glu Glu Ser Arg Gln Ala Arg  
50 55 60

Ile Thr Leu Gln Ser Val Asp Ala Arg Ala Leu Glu Leu Leu Ile Asp  
65 70 75 80

Tyr Val Tyr Thr Ala Thr Val Glu Val Asn Glu Asp Asn Val Gln Val  
85 90 95

Leu Leu Thr Ala Ala Asn Leu Leu Gln Leu Thr Asp Val  
100 105

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 105 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gln Leu Gln Asn Pro Ser His Pro Thr Gly Leu Leu Cys Lys Ala Asn  
1 5 10 15  
Gln Met Arg Leu Ala Gly Thr Leu Cys Asp Val Val Ile Met Val Asp  
20 25 30  
Ser Gln Glu Phe His Ala His Arg Thr Val Leu Ala Cys Thr Ser Lys  
35 40 45  
Met Phe Glu Ile Leu Phe His Arg Asn Ser Gln His Tyr Thr Leu Asp  
50 55 60  
Phe Leu Ser Pro Lys Thr Phe Gln Gln Ile Leu Glu Tyr Ala Tyr Thr  
65 70 75 80  
Ala Thr Leu Gln Ala Lys Ala Glu Asp Leu Asp Asp Leu Leu Tyr Ala  
85 90 95  
Ala Glu Ile Leu Glu Ile Glu Tyr Leu  
100 105

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 110 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Cys Leu Gln Phe Thr Arg His Ala Ser Asp Val Leu Leu Asn Leu Asn  
1 5 10 15  
Arg Leu Arg Ser Arg Asp Ile Leu Thr Asp Val Val Ile Val Val Ser  
20 25 30  
Arg Glu Gln Phe Arg Ala His Lys Thr Val Leu Met Ala Cys Ser Gly  
35 40 45  
Leu Phe Tyr Ser Ile Phe Thr Asp Gln Leu Lys Cys Asn Leu Ser Val  
50 55 60

Ile Asn Leu Asp Pro Glu Ile Asn Pro Glu Gly Phe Cys Ile Leu Leu  
65 70 75 80

Asp Phe Met Tyr Thr Ser Arg Leu Asn Leu Arg Glu Gly Asn Ile Met  
85 90 95

Ala Val Met Ala Thr Ala Met Tyr Leu Gln Met Glu His Val  
100 105 110